

O/PE

2/3/2001

Serial Number: 09/865,993

CRF Processing Date:

Edited by:

Verified by: (STIC staff)

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☒ Deleted extra, invalid, headings used by an applicant, specifically: C2207 in seq. 3
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/865,993

DATE: 07/03/2001

TIME: 17:21:54

Input Set : A:\Pto.amc

Output Set: N:\CRF3\07032001\I865993.raw

6 <110> APPLICANT: Brett P. Monia
7 Andrew T. Watt
9 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 5
EXPRESSION
11 <130> FILE REFERENCE: RTS-0175
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/865,993
C--> 13 <141> CURRENT FILING DATE: 2001-05-25
13 <160> NUMBER OF SEQ ID NOS: 89
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 20
18 <212> TYPE: DNA
19 <213> ORGANISM: Artificial Sequence
21 <220> FEATURE:
23 <223> OTHER INFORMATION: Antisense Oligonucleotide
25 <400> SEQUENCE: 1
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29 <210> SEQ ID NO: 2
30 <211> LENGTH: 20
31 <212> TYPE: DNA
32 <213> ORGANISM: Artificial Sequence
34 <220> FEATURE:
36 <223> OTHER INFORMATION: Antisense Oligonucleotide
38 <400> SEQUENCE: 2
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45 <213> ORGANISM: Homo sapiens
48 <220> FEATURE:
49 <221> NAME/KEY: CDS
50 <222> LOCATION: (47)...(1201)
52 <400> SEQUENCE: 3
53 cgcggggcgc gcggcgcggg gcggcctggc cggcgggcggc ggcggc atg aag gtc 55
54 Met Lys Val
55 1
57 acg tcg ctc gac ggg cgc cag ctg cgc aag atg ctc cgc aag gag gcg 103
58 Thr Ser Leu Asp Gly Arg Gln Leu Arg Lys Met Leu Arg Lys Glu Ala
59 5 10 15
61 gcg gcg cgc tgc gtg gtg ctc gac tgc cgg ccc tat ctg gcc ttc gct 151
62 Ala Ala Arg Cys Val Val Leu Asp Cys Arg Pro Tyr Leu Ala Phe Ala
63 20 25 30 35
65 gcc tcg aac gtg cgc ggc tcg ctc aac gtc aac ctc aac tcg gtg gtg 199
66 Ala Ser Asn Val Arg Gly Ser Leu Asn Val Asn Leu Asn Ser Val Val
67 40 45 50
69 ctg cgg cgg gcc cgg ggc ggc gcg gtg tcg gcg cgc tac gtg ctg ccc 247
70 Leu Arg Arg Ala Arg Gly Gly Ala Val Ser Ala Arg Tyr Val Leu Pro
71 55 60 65
73 gac gag gcg gcg cgc gcg cgg ctc ctg cag gag ggc ggc ggc ggc gtc 295

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| 74 | Asp | Glu | Ala | Ala | Arg | Ala | Arg | Leu | Gln | Glu | Gly | Gly | Gly | Gly | Val | |
| 75 | | | 70 | | | | | 75 | | | | 80 | | | | |
| 77 | gcg | gcc | gtg | gtg | gtg | ctg | gac | cag | ggc | agc | cgc | cac | tgg | cag | aag | ctg |
| 78 | Ala | Ala | Val | Val | Val | Leu | Asp | Gln | Gly | Ser | Arg | His | Trp | Gln | Lys | Leu |
| 79 | | | 85 | | | | | 90 | | | | 95 | | | | |
| 81 | cga | gag | gag | agc | gcc | gcg | cgt | gtc | gtc | ctc | acc | tcg | cta | ctc | gct | tgc |
| 82 | Arg | Glu | Glu | Ser | Ala | Ala | Arg | Val | Val | Leu | Thr | Ser | Leu | Leu | Ala | Cys |
| 83 | 100 | | | | | 105 | | | | | 110 | | | | 115 | |
| 85 | cta | ccc | gcc | ggc | ccg | cgg | gtc | tac | ttc | ctc | aaa | ggg | gga | tat | gag | act |
| 86 | Leu | Pro | Ala | Gly | Pro | Arg | Val | Tyr | Phe | Leu | Lys | Gly | Gly | Tyr | Glu | Thr |
| 87 | | | | | | 120 | | | | | 125 | | | | 130 | |
| 89 | ttc | tac | tcg | gaa | tat | cct | gag | tgt | tgc | gtg | gat | gta | aaa | ccc | att | tca |
| 90 | Phe | Tyr | Ser | Glu | Tyr | Pro | Glu | Cys | Cys | Val | Asp | Val | Lys | Pro | Ile | Ser |
| 91 | | | | 135 | | | | | | 140 | | | | 145 | | |
| 93 | caa | gag | aag | att | gag | agt | gag | aga | gcc | ctc | atc | agc | cag | tgt | gga | aaa |
| 94 | Gln | Glu | Lys | Ile | Glu | Ser | Glu | Arg | Ala | Leu | Ile | Ser | Gln | Cys | Gly | Lys |
| 95 | | | 150 | | | | | 155 | | | | | 160 | | | |
| 97 | cca | gtg | gta | aat | gtc | agc | tac | agg | cca | gct | tat | gac | cag | ggg | ggc | cca |
| 98 | Pro | Val | Val | Asn | Val | Ser | Tyr | Arg | Pro | Ala | Tyr | Asp | Gln | Gly | Gly | Pro |
| 99 | | | 165 | | | | | 170 | | | | | 175 | | | |
| 101 | gtt | gaa | atc | ctt | ccc | ttc | ctc | tac | ctt | gga | agt | gcc | tac | cat | gca | tcc |
| 102 | Val | Glu | Ile | Leu | Pro | Phe | Leu | Tyr | Leu | Gly | Ser | Ala | Tyr | His | Ala | Ser |
| 103 | 180 | | | | | 185 | | | | | 190 | | | | 195 | |
| 105 | aag | tgc | gag | ttc | ctc | gcc | aac | ttg | cac | atc | aca | gcc | ctg | ctg | aat | gtc |
| 106 | Lys | Cys | Glu | Phe | Leu | Ala | Asn | Leu | His | Ile | Thr | Ala | Leu | Leu | Asn | Val |
| 107 | | | | 200 | | | | | | 205 | | | | 210 | | |
| 109 | tcc | cga | cgg | acc | tcc | gag | gcc | tgc | atg | acc | cac | cta | cac | tac | aaa | tgg |
| 110 | Ser | Arg | Arg | Thr | Ser | Glu | Ala | Cys | Met | Thr | His | Leu | His | Tyr | Lys | Trp |
| 111 | | | | 215 | | | | | | 220 | | | | 225 | | |
| 113 | atc | cct | gtg | gaa | gac | agc | cac | acg | gct | gac | att | agc | tcc | cac | ttt | caa |
| 114 | Ile | Pro | Val | Glu | Asp | Ser | His | Thr | Ala | Asp | Ile | Ser | Ser | His | Phe | Gln |
| 115 | | | 230 | | | | | 235 | | | | | 240 | | | |
| 117 | gaa | gca | ata | gac | ttc | att | gac | tgt | gtc | agg | gaa | aag | gga | ggc | aag | gtc |
| 118 | Glu | Ala | Ile | Asp | Phe | Ile | Asp | Cys | Val | Arg | Glu | Lys | Gly | Gly | Lys | Val |
| 119 | | | 245 | | | | 250 | | | | | 255 | | | | |
| 121 | ctg | gtc | cac | tgt | gag | gct | ggg | atc | tcc | cgt | tca | ccc | acc | atc | tgc | atg |
| 122 | Leu | Val | His | Cys | Glu | Ala | Gly | Ile | Ser | Arg | Ser | Pro | Thr | Ile | Cys | Met |
| 123 | 260 | | | | | 265 | | | | | 270 | | | | 275 | |
| 125 | gct | tac | ctt | atg | aag | acc | aag | cag | ttc | cgc | ctg | aag | gag | gcc | ttc | gat |
| 126 | Ala | Tyr | Leu | Met | Lys | Thr | Lys | Gln | Phe | Arg | Leu | Lys | Glu | Ala | Phe | Asp |
| 127 | | | | 280 | | | | | | 285 | | | | 290 | | |
| 129 | tac | atc | aag | cag | agg | agg | agc | atg | gtc | tcg | ccc | aac | ttt | ggc | ttc | atg |
| 130 | Tyr | Ile | Lys | Gln | Arg | Arg | Ser | Met | Val | Ser | Pro | Asn | Phe | Gly | Phe | Met |
| 131 | | | | 295 | | | | | 300 | | | | | 305 | | |
| 133 | ggc | cag | ctc | ctg | cag | tac | gaa | tct | gag | atc | ctg | ccc | tcc | acg | ccc | aac |
| 134 | Gly | Gln | Leu | Leu | Gln | Tyr | Glu | Ser | Glu | Ile | Leu | Pro | Ser | Thr | Pro | Asn |
| 135 | | | 310 | | | | | 315 | | | | | 320 | | | |
| 137 | ccc | cag | cct | ccc | tcc | tgc | caa | ggg | gag | gca | gca | ggc | tct | tca | ctg | ata |
| 138 | Pro | Gln | Pro | Pro | Ser | Cys | Gln | Gly | Glu | Ala | Ala | Gly | Ser | Ser | Leu | Ile |

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Input Set : A:\Pto.amc

Output Set: N:\CRF3\07032001\I865993.raw

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143 340      345      350      355
145 ttc cct gcc tcg gtg ctg gca ccg gtg cct acc cac tca aca gtc tca      1159
146 Phe Pro Ala Ser Val Leu Ala Pro Val Pro Thr His Ser Thr Val Ser
147      360      365      370
149 gag ctc agc aga agc cct gtg gca acg gcc aca tcc tgc taa aactgggatg 1211
150 Glu Leu Ser Arg Ser Pro Val Ala Thr Ala Thr Ser Cys
W--> 151      375      380      385
153 gaggaatcgg cccagcccca agagcaactg tgatttttgt ttttaagact catggacatt 1271
155 tcatacctga tgcaatactg aagacctcat tctgtcatgc tgccccagtg agatagttag 1331
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159 ggaaggccaa gccattacgg gagcacagca tgtgtgtgact actgtacttc cagacccttg 1451
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163 gcaataaata cctgcagcaa cgtgggagaa agaagttgct ggaccaggag aaaaggcagt 1571
165 tatgaagcca attcattttg aaggaagcac aatttccacc ttattttttg aactttggca 1631
167 gtttcaatgt ctgtctctgt tgcttcgggg cataagctga tcaccgtcta gttgggaaag 1691
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173 tggatttttt ttgccatggg ttcttctact accttgact ttggcatgat tcttagtcat 1871
175 acttgaactt gtctcattcc acctctctc agagcaactc ttcctttggg aaaagagttc 1931
177 ttcagatcat agaccataaa agtcatacct tcgaggtggt agcagtagat tccaggagga 1991
179 gaagggtact tgctaggtat cctgggtcag tggcggtgca aactggtttc ctcagctgcc 2051
181 tgtccttctg tgtgcttatg tctcttgtga caattgtttt cctccctgcc cctggaggtt 2111
183 gtcttcaagc tgtggacttc tgggattt      2139
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189 <213> ORGANISM: Artificial Sequence
191 <220> FEATURE:
193 <223> OTHER INFORMATION: PCR Primer
195 <400> SEQUENCE: 4
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199 <210> SEQ ID NO: 5
200 <211> LENGTH: 25
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214 <212> TYPE: DNA
215 <213> ORGANISM: Artificial Sequence
217 <220> FEATURE:
219 <223> OTHER INFORMATION: PCR Probe
221 <400> SEQUENCE: 6

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239 <211> LENGTH: 20
240 <212> TYPE: DNA
241 <213> ORGANISM: Artificial Sequence
243 <220> FEATURE:
245 <223> OTHER INFORMATION: PCR Primer
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253 <212> TYPE: DNA
254 <213> ORGANISM: Artificial Sequence
256 <220> FEATURE:
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283 gccctatctg gccttcgctg cctcgaacgt gcgcggctcg ctcaacgtca acctcaactc 360
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303 tgtggaagac agccacacgg ctgacattag ctcccacttt caagaagcaa tagacttcat 960
305 tgactgtgtc agggaaaagg gaggcaaggt cctggtccac tgtgaggctg ggatctcccg 1020
307 ttcacccacc atctgcatgg cttaccttat gaagaccaag cagttccgcc tgaaggaggc 1080

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Input Set : A:\Pto.amc

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313 ccaaggggag gcagcaggct cttaactgat aggccatttg cagacactga gccctgacat 1260
315 gcaggggtgcc tactgcacat tccctgcttc ggtgctggca ccggtgccta cccactcaac 1320
317 agtctcagag ctacgcagaa gccctgtggc aacggccaca tcctgctaaa actgggatgg 1380
319 aggaatcggc ccagcccca gagcaactgt gatttttgtt ttaagactc atggacattt 1440
321 catacctgat gcaatactga agacctcatt ctgtcatgct gccccagtga gatagtgagt 1500
323 ggtcaccagg cttgcaaattg aacttcagac ggacctcagg gtaggttctc gggactgaag 1560
325 gaaggccaag ccattacggg agcacagcat gtgctgacta ctgtacttcc agaccctgc 1620
327 cctcttgga ctgcccagtc cttgcacctc agagttcgcc ttttcatttc aagcataagg 1680
329 caataaatac ctgcagcaac gtgggagaaa gaagttgctg gaccaggaga aaaggcagtt 1740
331 atgaagccaa ttcattttga aggaagcaca atttccacct tattttttga actttggcag 1800
333 tttcaatgtc tgtctctgtt gcttcggggc ataagctgat caccgtctag ttgggaaagt 1860
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337 tagacaccct cttgggtcca atgaggtagt tggttgaagt agcaagatgt tggcttttct 1980
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343 tcagatcata gacaaaaaaa gtcataacct cgaggtggtg gcagtagatt ccaggaggag 2160
345 aagggtactt gctaggtatc ctgggtcagt ggcggtgcaa actggtttcc tcagctgcct 2220
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359 <211> LENGTH: 475

360 <212> TYPE: DNA

361 <213> ORGANISM: Homo sapiens

363 <220> FEATURE:

366 <400> SEQUENCE: 11

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371 ggcatgaagg tcaagtcgct cgacgggcgc cagctgcgca agatgctccg caaggaggcg 180
373 gcgcgcgct gcgtggtgct cgactgccgc cctatctggt ccttcgctgc ctgaacgtg 240
375 cgcggctcgc tcaacgtcaa cctcaactcg gtggtgctgc ggcgggcccg ggcgggcgcg 300
377 gtgtcggcgc gctacgtgct ggaccagggc agccgccact ggcagaagct gcgagaggag 360
379 agcgcgcgc gtgtcgtcct caccctgcta ctgcttgcc taccgcgcg cccgcgggtc 420
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385 <211> LENGTH: 20

386 <212> TYPE: DNA

387 <213> ORGANISM: Artificial Sequence

389 <220> FEATURE:

391 <223> OTHER INFORMATION: Antisense Oligonucleotide

393 <400> SEQUENCE: 12

394 gacgtgacct tcatgccgcc

20

397 <210> SEQ ID NO: 13

398 <211> LENGTH: 20

399 <212> TYPE: DNA

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:151 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3